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In the Claims:

Please amend claims 35, 39 and 40 as follows:

1. (Original) A method of controlling cancer suppression in a mammal having a cancer suppressing gene, comprising the steps of:

making a substantially duplicated genetic material corresponding to the genetic material of said gene, the substantially duplicated material selected from the group consisting of a cloned cancer suppressing gene, a modified or defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof; and

interchanging said duplicated genetic material and the cancer suppressing gene of the mammal.

2. (Original) A method of claim 1, wherein before said making a substantially duplicated genetic material, determining the chromosomal location of said cancer suppressing gene of the mammal.

3. (Original) A method of claim 1, wherein after said making a substantially duplicated genetic material, detecting the presence or absence of an inactive cancer suppressing gene of a tissue sample of the mammal to determine whether or not the tissue sample cancer suppressing gene is defective or absent.

4. (Original) A method of claim 3, wherein in response to a determination that the tissue sample cancer suppressing gene is either defective or absent, replacing a cancer suppressing gene of the mammal with its clone.

5. (Original) A method of claim 3, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by measuring the amount of protein product of said cancer suppressing gene, of the tissue sample, bound by an antibody specific for said protein.

6. (Original) A method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by:

- (a) labeling said tissue sample with radioactive isotope;
- (b) lysing the labeled tissue;
- (c) reacting the protein product of said cancer suppressing gene with an antibody specific for said protein thereby forming a protein/antibody immunocomplex;
- (d) autoradiographing the immunocomplex obtained in step (c); and
- (e) determining the presence or absence of the protein product by comparing the autoradiogram of step (d) with the autoradiogram of the standard protein product.

7. (Original) The method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by enzyme immunoassay techniques.

8. (Original) The method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by immunocytochemistry methods.

9. (Original) The method of claim 5, wherein the cancer suppressing gene is the RB gene and the protein product is ppRB¹¹⁰.

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10. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said cloned cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for therapeutic purposes.

11. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for facilitating the testing of the carcinogenicity of environmental influences.

12. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined by chromosome walking.

13. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined through organic markers.

14. (Original) A method of claim 2, wherein:
said chromosomal location of said cancer suppressing gene is determined by testing genes of a chromosome for phenotypic expression;
determining one of the genes of said chromosome to be a marker gene; and
using chromosomal walking techniques to locate a cancer suppressing gene.

15. (Original) An animal genetically altered so as to have the allele of at least one cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof.

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16. (Original) An animal of claim 15, wherein said defective allele is selected from the group consisting of defective alleles of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

17. (Original) An animal of claim 15, wherein said allele contains a DNA fragment having at least one defective nucleotide sequence.

18. (Original) An animal of claim 15, wherein said defective allele contains a DNA fragment having at least one defective RB nucleotide sequence.

19. (Original) The animal of claim 15, wherein said animal is a mouse.

20. (Original) A method for determining the carcinogenicity of suspected environmental influences, using the animal of claim 14, comprising the steps of:
exposing said animal to a suspected environmental influence;
observing the animal for the phenotypic expression of cancer; and
determining carcinogenicity of the suspected environmental influence in response to observing a phenotypic expression of cancer in the animal.

21. (Original) A method of claim 20, wherein said exposing includes exposing to a source of radiation.

22. (Original) A method of claim 20, wherein said exposing includes exposing to tobacco combustion products.

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23. (Original) A method of claim 20, wherein said exposing includes exposing to food additives.

24. (Original) A method of claim 20, wherein said exposing includes exposing to artificial substances.

25. (Original) A method of claim 20, wherein said observing includes examining the animal for tumor development.

26. (Original) A method of claim 25, wherein in response to the formation of a tumor in the animal, analyzing the tumor for the presence of cancer cells.

27. (Original) A method of making the animal of claim 15, comprising: using at least one allele of an animal cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof;

mutating at least one animal cell with said allele to form a mutated cell; introducing said mutated cell into an animal blastocyst;

permitting growth of the blastocyst for a given period of time sufficient to incorporate said allele into its cells; repressing genetic recombinations within said cells; transferring the blastocyst containing said allele into the uterus of a pseudo pregnant animal for giving birth subsequently to an animal bearing said allele;

breeding said animal to reproduce additional animals; and selecting the animal of claim 14 from said additional animals by determining the presence therein of the said allele.

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28. (Original) A method of claim 27, wherein before introducing said allele, removing said blastocyst from a super ovulated animal, and wherein said blastocyst is comprised of undifferentiated cells.

29. (Original) A method of claim 27, wherein said introducing is performed in vitro.

30. (Original) A pharmaceutical composition wherein the active ingredient is selected from the group consisting of a naturally occurring intact cancer suppressing gene, a cloned intact cancer suppressing gene, fragments thereof, homologues thereof and mixtures thereof.

31. (Original) A pharmaceutical composition of claim 30, wherein said naturally occurring and cloned cancer suppressing gene is selected from the group consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

32. (Original) A pharmaceutical composition of claim 30, wherein the active ingredient is selected from the group consisting of RB cDNA, modified RB cDNA fragment, clones thereof, homologues thereof and mixtures thereof.

33. (Original) A pharmaceutical composition of claim 31, wherein the active ingredient for each of said gene is selected from the group consisting of cDNA of said gene, fragments of said cDNA, homologues thereof and mixtures thereof.

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34. (Original) A pharmaceutical composition of claim 32, wherein the cancer suppressing gene is isolated from human chromosome 13 region 13q14.

35. (Currently amended) A pharmaceutical composition of claim 31, wherein the cancer suppressing gene and its clone each has the following nucleotide sequence comprising SEQ ID NO:1:

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TTCCGGTTTT TCTCAGGGCA CGTTGAAATT ATTTTGTA CGGGACTCGG CACAGGACGG 60
cccccccccc cccctggggcc cccctccctt cccggggctt cctccacagg tccctggctc 120
ccccccccccaa AACGGGTC ATG CCC CCC AAA ACC CCC CGA AAA ACG CCC CCC 171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10

ACC CCC CCC CCT CCC CCC GCG GAA CCC CCC CGA CCC CCC CCC CCC CCC 219
Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
15 20 25

CCT CCC TAG GAC GAC CCA GAG CAG GAC AGC GGC CCC GAG GAC CTC CCT 267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40

CTC GTC AGC CTT GAC TTT GAA GAA ACA GAA GAA CCT CAT TTT ACT GCA 315
Leu Val Arg Leu Glu Phe Glu Clu Thr Clu Glu Pro Asp Phe Thr Ala
45 50 55

TTA TGT CAC AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA CCT TGC 363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75

TTA ACT TGC GAC AAA CTT TCA TCT GTC CAT CGA CTA TTC GGA CGT TAT 411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90

ATT CAA AAC AAA AAC GAA CTG TGC GGA ATC TGT ATC TTT ATT CCA GCA 459
Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105

CTT CAC CTA CAT GAG ATC TCG TTC ACT TTT ACT GAC CTA CAG AAA AAC 507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
110 115 120

ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT 555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135

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ACC ACT ACC AAA GTT GAT AAT CCT ATG TCA AGA CTG TTC AAG AAG TAT 603
 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
 140 . 145 150 155

GAT GTA TTG TTT GCA CTC TTC ACC AAA TTG GAA AGG ACA TGT CAA CTT 651
 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
 160 165 170

ATA TAT TTG ACA CAA CCC ACC ACT TCG ATA TCT ACT CAA ATA AAT TCT 699
 Ile Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser
 175 180 185

GCA TTG CTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG 747
 Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
 190 195 200

GAA GTA TTA CAA ATG CAA GAT CAT CTC CTG ATT TCA TTT CAG TTA ATG 795
 Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
 205 210 215

CTA TCT CTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843
 Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
 220 225 230 235

AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT CCT TCA CCT CGA 891
 Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
 240 245 250

ACA CCC ACC CGA CGT CAG AAC ACC ACT CGA CGG ATA CGA AAA CAA CTA 939
 Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
 255 260 265

GAA AAT GAT ACA ACA ATT ATT CAA GTT CTC TGT AAA GAA CAT CAA TCT 987
 Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
 270 275 280

AAT ATA GAT CAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT 1035
 Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
 285 290 295

ATG AAT TCT CTT CGA CTT CTA ACA TCT AAT CGA CTT CCA GAG CTT GAA 1083
 Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
 300 305 310 315

AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA CAT CTA 1131
 Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
 320 325 330

GAT CGA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179
 Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
 335 340 345

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ATA GAC ACT TTT GAA ACA CAG AGA ACA CCA CCA AAA ACT AAC CTT CAT 1227
 Ile Asp Ser Phe Glu Thr Cln Arg Thr Pro Arg Lys Ser Asn Leu Asp
 350 355 360

GAA GAC GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGC ACT GTT ATC 1275
 Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
 365 370 375

AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA CCA ACT CAT CAA 1323
 Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
 380 385 390 395

CCT TCA GAA AAT CTC ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA 1371
 Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
 400 405 410

AAA GAA AGT ATA CTG AAA ACA GTG AAG GAT ATA GGA TAC ATC TTT AAA 1419
 Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys
 415 420 425

GAG AAA TTT CCT AAA CCT GTG CCA CAG CGT TGT CTC GAA ATT CCA TCA 1467
 Glu Lys Phe Ala Lys Ala Val Gly Cln Gly Cys Val Glu Ile Gly Ser
 430 435 440

CAC CGA TAC AAA CTT CGA CTT CGC TTG TAT TAC CGA GTC ATG GAA TCC 1515
 Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser
 445 450 455

ATG CTT AAA TCA GAA CAA GAA CGA TTA TCC ATT CAA AAT TTT ACC AAA 1563
 Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys
 460 465 470 475

CTT CTG AAT GAC AAC ATT TTT CAT ATC TCT TTA TTG CGG TGC CCT CTT 1611
 Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu
 480 485 490

GAG CTT GTC ATG GCC ACA TAT AGC ACA ACT ACA TCT CAG AAT CTT CAT 1659
 Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp
 495 500 505

TCT CGA ACA GAT TTG TCT TTC CCA TGC ATT CTG AAT GTC CTT AAT TTA 1707
 Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu
 510 515 520

AAA CCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA 1755
 Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu
 525 530 535

CCC AAC TTG ACA ACA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT 1803
 Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His
 540 545 550 555

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CGA ATC ATG CAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT CAT 1851
 Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
 560 565 570

CTT ATT AAA CAA TCA AAC GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA 1899
 Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
 575 580 585

TCT CCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA 1947
 Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
 590 595 600

GAT ATC TAT CTT TCT CCT CTA AGA TCT CCA AAC AAA AAA GGT TCA ACT 1995
 Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Gly Ser Thr
 605 610 615

ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA CCC 2043
 Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
 620 625 630 635

TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT 2091
 Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
 640 645 650

AAA AAA CTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TCT GAA 2139
 Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
 655 660 665

CCC CTT CTG TCT GAG CAC CCA CAA TTA CAA CAT ATC ATC TGG ACC CTT 2187
 Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
 670 675 680

TTC CAG CAC ACC CTC CAG AAT CAG TAT GAA CTC ATG AGA GAC AGG CAT 2235
 Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
 685 690 695

TTG GAC CAA ATT ATG ATC TGT TCC ATG TAT GGC ATA TGC AAA GTC AAG 2283
 Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
 700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT 2331
 Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
 720 725 730

CCT CAT GCT GTT GAG CAG ACA TTC AAA CGT GTT TTG ATC AAA CAA GAG 2379
 Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
 735 740 745

GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA 2427
 Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Cln Arg
 750 755 760

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CTG AAA ACA AAT ATT TTG CAG TAT CCT TCC ACC AGG CCC CCT ACC TTC 2475
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu
765 770 775

TCA CCA ATA CCT CAC ATT CCT CGA ACC CCT TAC AAG TTT CCT AGT TCA 2523
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
780 785 790 795

CCC TTA CGG ATT CCT CGA CGG AAC ATC TAT ATT TCA CCC CTC AAG AGT 2571
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
800 805 810

CCA TAT AAA ATT TCA CAA CCT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
815 820 825

AGA TCA AGA ATC TTA CTA TCA ATT CCT GAA TCA TTC CGG ACT TCT GAG 2667
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
830 835 840

AAG TTC CAC AAA ATA AAT CAG ATG GTC TGT AAC ACC GAC CGT CTC 2715
Lys Phe Glu Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
845 850 855

AAA AGA AGT CCT GAA GGA ACC AAC CCT CCT AAA CCA CTG AAA AAA CTA 2763
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
860 865 870 875

CCC TTT CAT ATT GAA CGA TCA CAT GAA CGA GAT CGA ACT AAA CAT CTC 2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
880 885 890 895

CCA CGA GAG TCC AAA TTT CAG CAG AAA CTG CGA GAA ATG ACT TCT ACT 2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
895 900 905

CGA ACA CGA ATG GAA AAC CAG AAA ATG AAT GAT ACC ATG GAT ACC TCA 2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
910 915 920

AAC AAC GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT 2962
Asn Lys Glu Glu Lys
925

GGATTCATTC TCTCTGACAG ATGTCAGTGT AT 2994

36. (Original) A pharmaceutical composition of claim 32, wherein said RB cDNA fragment is selected from the group consisting of RB-1, RB-2, RB-5, γ 79R8 and mixtures thereof.

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37. (Original) A pharmaceutical composition of claim 32, wherein a resulting mRNA transcript of said RB cDNA fragment has 4.6 kb.

38. (Original) A pharmaceutical composition of claim 37, wherein the cloned genomic DNA has at least 27 exons.

39. (Currently amended) A pharmaceutical composition of claim 30, wherein the cloned RB cDNA transcribes into mRNA which translates in protein having an amino acid sequence comprising SEQ ID NO:2:

~~MPPKTPRKTAAATAAAAAEPPAPPPPPPPEEDPE (34)~~
~~QDSCGPEDLPLVRLFEFETEEDFTALCQKLKIPDHVRERA (74)~~
~~WL TW EKVSSV DGV LGGYI QKK KELWGICIFIAAVD LDEM S (114)~~
~~FTFT EQL QNIEI SVHKFFNLLKEIDTSTKVDNAMS RLLKK (154)~~
~~YDVL FALFS KLER TCELI YLTQ PSS SISTE I NSALV LKV S (194)~~
~~WITF LLA KGEV LQMED DLV I S FQL NLCV LDYF I KLS PPM L (234)~~
~~LKEPYKTAVI PINGSPRT PRRGQMRSARIAKQLENDTRI I (274)~~
~~EVLCKEHECN I D E V K N V Y F K N F I P F M N S L G L V T S N C L P E V (314)~~
~~ENLS KRYEE I Y L K N K D L D A R L F L D H D K T L Q T D S I D S F E T Q (354)~~
~~RTPR K S N L D E E V N V I P P H T P V R T V M N T I Q Q L M M I L N S A S D (394)~~
~~Q PSEN L I S Y F N N C T V N P K E S I L K R V K D I C Y I F K E K F A K A V (434)~~
~~GQCC V E I G S Q R Y K L G V R L Y Y R V M E S M L K S E E R L S I Q N F S (474)~~
~~K L N D N I F H M S I L L A C A L E V V M A T Y S R S T S Q N L D S G T D L S F (514)~~
~~P W I L N V I N L K A F D F Y K V I E S F I K A E C N L T R E M I K H L E R C E (554)~~
~~H R I M E S I A W I L S D S P L F D L I K Q S K D R E C P T D H L E S A C P L N L (594)~~
~~P L Q N N H T A A D M Y L S P V R S P K K K G S T T R V N S T A N A E T Q A T S (634)~~
~~A F Q T Q K P L K S T S L S L F Y K K V Y R A Y L R L N T L C E R L L S E H P (674)~~
~~E L E H I I W T L F Q H T L Q N E Y E L M R D R H I L D Q I M M C S M Y G I C K V (714)~~
~~K N I D L K F K I I V T A Y K D L P H A V Q E T F K R V L I K E E Y D S I I V (754)~~
~~F Y N S V F M Q R I K T N I L Q Y A S T R P P T L S P I P H I P R S P Y K F P S (794)~~
~~S P L R I P G C N I Y I S P L K S P Y K I S E G L P T P T K M T P R S R I L V S (834)~~
~~I C E S F G T S E K F Q K I N Q M V C N S D R V L K R S A E G S N P P K P L K K (874)~~
~~L R F D I E G S D E A D G S K H L P G E S K F Q Q K L A E M T S T R T R M Q K Q (914)~~
~~K M N D S M D T S N K E E K (928)~~

~~single letter abbreviations for the amino acid residues are:~~
~~A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;~~

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~~I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;~~
~~R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.~~

40. (Currently amended) A DNA nucleotide sequence comprising SEQ
ID NO:1.

TTCGGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTA CGGGACTCGG GAGAGGACGG 60
 CCCGTCCCCC CCCTCCCCCC CGCTCGTCCT CCCCCGGGCT CCTCCACAGC TCGCTGGCTC 120
 CCCCCGGGAA AAGCCGTC ATG CCC CCC AAA ACC CCC CGA AAA AGG CCC GCC 171
 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
 1 5 10

 ACC CCC CCC CCT CCC CCC GCG GAA CCC CCC CCA CCC CCG CCC CCC CCC 219
 Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
 15 20 25

 CCT CCG TAG CAG GAC CCA GAG CAG GAC ACC CCC CCG GAG GAC CTG CCT 267
 Pro Pro Glu Glu Asp Pro Glu Cln Asp Ser Gly Pro Glu Asp Leu Pro
 30 35 40

 CTC GTC AGC CTT GAG TTT GAA CAA ACA GAA GAA CCT CAT TTT ACT CCA 315
 Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Pro Asp Phe Thr Ala
 45 50 55

 TTA TGT CAG AAA TTA AAC ATA CCA GAT CAT GTC AGA GAG AGA CCT TGG 363
 Leu Cys Cln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
 60 65 70 75

 TTA ACT TCG CAG AAA CTT TCA TCT GTC GAT GGA CTA TTC GGA CCT TAT 411
 Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
 80 85 90

 ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA 459
 Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
 95 100 105

 CTT GAC CTA GAT GAG ATC TCG TTC ACT TTT ACT GAG CTA CAC AAA AAC 507
 Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
 110 115 120

 ATA GAA ATC ACT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT 555
 Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
 125 130 135

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ACC ACT ACC AAA GTT GAT AAT CCT ATG TCA AGA CTG TTG AAC AAG TAT 603
 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
 140 145 150 155

GAT GCA TTG TTT GCA CTC TTC ACC AAA TTG GAA AGG ACA TGT CAA CTT 651
 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
 160 165 170

ATA TAT TTG ACA CAA CCC ACC ACT TCG ATA TCT ACT CAA ATA AAT TCT 699
 Ile Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser
 175 180 185

GCA TTG CTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGC 747
 Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
 190 195 200

GAA GTA TTA CAA ATG CAA GAT CAT CTG CTG ATT TCA TTT CAG TTA ATG 795
 Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
 205 210 215

CTA TCT CTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843
 Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
 220 225 230 235

AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT CCT TCA CCT CGA 891
 Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
 240 245 250

ACA CCC AGG CCA CGT CAC AAC ACC ACT CCA CCC ATA CCA AAA CAA CTA 939
 Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
 255 260 265

GAA AAT GAT ACA AGA ATT ATT CAA GTT CTC TGT AAA CAA CAT GAA TGT 987
 Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
 270 275 280

AAT ATA GAT GAG GTG AAA AAT CTT TAT TTC AAA AAT TTT ATA CCT TTT 1035
 Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
 285 290 295

ATG AAT TCT CTT CGA CTT GCA ACA TCT AAT GGA CTT CCA GAG GTT GAA 1083
 Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
 300 305 310 315

AAT CTT TCT AAA CGA TAC GAA CAA ATT TAT CTT AAA AAT AAA CAT CTA 1131
 Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
 320 325 330

GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179
 Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
 335 340 345

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ATA GAC ACT TTT GAA ACA CAG AGA ACA CCA CGA AAA ACT AAC CTT GAT 1227
 Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
 350 355 360

GAA GAG GTG AAT GCA ATT CCT CCA CAC ACT CCA GTT AGG ACT CTT ATG 1275
 Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
 365 370 375

AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT CAT CAA 1323
 Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
 380 385 390 395

GCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTC AAT CCA 1371
 Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
 400 405 410

AAA GAA AGT ATA CTG AAA AGA CTG AAC GAT ATA CGA TAC ATC TTT AAA 1419
 Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys
 415 420 425

GAG AAA TTT CCT AAA CCT GTC CGA CAG CGT TGT CTC GAA ATT CGA TCA 1467
 Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser
 430 435 440

CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTC ATG CAA TCC 1515
 Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser
 445 450 455

ATG CTT AAA TCA GAA CAA GAA CGA TTA TCC ATT CAA AAT TTT ACC AAA 1563
 Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys
 460 465 470 475

CTT CTC AAT GAC AAC ATT TTT CAT ATG TCT TTA TTC CGC TGC CCT CTT 1611
 Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu
 480 485 490

GAG GTT GTC ATG GCC ACA TAT ACC AGA ACT ACA TCT CAG AAT CTT GAT 1659
 Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp
 495 500 505

TCT CGA ACA GAT TTG TCT TTC CGA TGG ATT CTG AAT GTC CTT AAT TTA 1707
 Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu
 510 515 520

AAA CCC TTT CAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA CGA GAA 1755
 Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu
 525 530 535

GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT 1803
 Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His
 540 545 550 555

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CGA ATC ATG GAA TCC CTT GCA TCG CTC TCA GAT TCA CCT TTA TTT CAT 1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
560 565 570

CTT ATT AAA CAA TCA AAG GAC CGA GAA CGA ACT GAT GAC CTT CAA 1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
575 580 585

TCT CCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA CCA 1947
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
590 595 600

GAT ATC TAT CTT TCT CCT GCA AGA TCT CGA AAG AAA AAA GGT TCA ACT 1995
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
605 610 615

ACG CCT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA CCC 2043
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
620 625 630 635

TTC CAG ACC CAC AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT 2091
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
640 645 650

AAA AAA CTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TCT CAA 2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
655 660 665

CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT 2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
670 675 680

TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATC AGA GAC ACC GAT 2235
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
685 690 695

TTG CAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTC AAG 2283
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GCA ACA GCA TAC AAC GAT CTT 2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
720 725 730

CCT CAT GCT GTT CAG CAG ACA TTC AAA CGT CTT TTG ATC AAA CAA CAG 2379
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
735 740 745

GAG TAT GAT TCT ATT ATA GCA TTC TAT AAC TCG GTC TTC ATC CAG AGA 2427
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
750 755 760

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CTG AAA ACA AAT ATT TTG CAG TAT CCT TCC ACC AGG CCC CCT ACC TTG 2475
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu
765 770 775

TCA CCA ATA CCT CAC ATT CCT CGA ACC CCT TAC AAG TTT CCT AGT TCA 2523
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
780 785 790 795

CCC TTA CGG ATT CCT CGA CGG AAC ATC TAT ATT TCA CCC CTC AAC ACT 2571
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
800 805 810

CCA TAT AAA ATT TCA CAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
815 820 825

AGA TCA AGA ATC TTA GTC TCA ATT CCT CAA TCA TTC CGG ACT TCT CAG 2667
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
830 835 840

AAG TTC CAC AAA ATA AAT CAG ATG GTC TGT AAC AGC GAC CGT CTC 2715
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
845 850 855

AAA AGA AGT CCT GAA CGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA 2763
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
860 865 870 875

CCC TTT GAT ATT CAA CGA TCA GAT CAA CGA CAT CGA ACT AAA CAT CTC 2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
880 885 890

CCA CGA GAG TCC AAA TTT CAG CAG AAA CTG CGA GAA ATG ACT TCT ACT 2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
895 900 905

CGA ACA CGA ATG CAA AAC GAC AAA ATG AAT GAT ACC ATG CTC ACC TCA 2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
910 915 920

AAC AAC GAA GAG AAA TCAGGATCTC AGGACCTTGG TGGACACTGT CTACACCTCT 2962
Asn Lys Glu Glu Lys
925

GGATTCATTC TCTCTCACAG ATGTCAGTGT AT 2994

41. (Original) A method of therapeutically treating inactive, mutative or absent cancer suppressing genes comprising:

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treating said inactive, mutative or absent cancer suppressing genes with at least a portion of intact cancer suppressing genes.

42. (Original) A method of claim 41, wherein said cancer suppressing genes are each a substance selected from the groups consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, and mixtures thereof.

43. (Original) A method of claim 41, wherein said treating includes: treating said inactive, mutative or absent cancer suppressing gene with a substance selected from the group consisting of an RB gene, a portion of said gene, or a mixture thereof.

44. (Original) A method of claim 43, wherein said portion is selected from the group consisting of RB cDNA, RB cDNA fragment, homologues thereof and mixtures thereof.

45. (Original) The method of claim 41, wherein the intact cancer suppressing gene, or portion thereof, is delivered to the site of a tumor by means of a retrovirus.

46. (Original) A method of claim 41, wherein the intact cancer suppressing gene, or a portion thereof, is delivered to the site of a tumor by a liposome.

47. (Original) A method of claim 41, wherein the location of said cancer suppressing gene is determined by utilizing a genetic marker.